GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

No.

Score

Match Length DB

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Description

	Run on:	OM nucleic -
(without alignments) 6623.439 Million cell updates/sec	August 24, 2004, 17:45:39 ; Search time 4175 Seconds	OM nucleic - nucleic search, using s⊌ model

Scoring table: IDENTITY_NUC Gapop 10.0 .	Title: US- Perfect score: 638 Sequence: 1 g
IDENTITY NUC Gapop 10.0 , Gapext 1.0	US-10-022-554A-3 638 1 gaattegggaaegegecacacetgaatttgtmageaactt 638

Post-processing: Minimum Match 0%	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Total number of hits satisfying chosen parameters:
	•	6940544

Searched

3470272 seqs, 21671516995 residues

		Database :	Post-processing:
12: 9b_gv:" 13: 9b_gv:" 14: 9b_vi:" 15: em_ba:" 16: em_fun:" 17: em_fun:" 18: em_fun:" 20: em_mu:" 21: em_ov:"	2. 9b htg:* 3. 9b in: 4. 9b_on: 5. 9b pat:* 6. 9b pat:* 7. 9b pat:* 9. 9b pat:* 9. 9b pat:* 11. ob fr:*	GenEmbl;* 1. gb_ba;*	Minimum Watch 0% Maximum Match 100% Listing first 45 summaries

	.	40.	39,	38.	37:	36.	35-	14.	35:	32:) ·			29.	20:	27:	26:	25:	24:	2.51	2 1	22:	21:	20:	19:	18:	17:	16:	15:	14:	13:	12:	111	10:	9-	<u>.</u>	7.	σ.	5.	4
1		htgo	em_htgo_hum:*	em_8y:*	em_htg_vrt:*	nam:	rod	urd bru	em_htg_mus:*	ncg_othe	reg_anv:	The state of the s	:	- T	em un:*	cm sts:*	em_ro;*	em_pl:*	em_ph:*	em_pac.		em ov.*	em or:	em om: *	em_mu:*	em_in.*	em_hum:*	em_fun:*	em ba:*	gb_v1:*	gb_un:*	gb_sy:*	gb_sts:*	gb_ro:*	gb_pr:*	95,51:	gb_ph. •	gb_pat: *	gb_ov.*	gb_om: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being print and is derived by analysis of the total score distribution.

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	b	ij

Query

Result

REFERENCE 1 (bases I to 638) AUTHORS Jaye, M., Burgess, W., Maciag, T. and Drohan, W. TITLE Recombinant DNA vector encoding human endoth factor	RESULT 1 102042 638 bp 88-DNA LOCUS 102042 From Patent US 4868113. ACCESSION 102042 Patent US 4868113. VERSION 102042.1 GI:270417 KEYMORDS Unknown. OMCANISM Unknown.	72.7 481 6 72.6 468 6 468 6 468 10 68.1 2507 10 68.1 2507 10 66.2 472 472 472 472 472 472 472 472 472 47	9 485.2 76.1 490 6 10 485.2 76.1 480 9 11 474.2 74.3 668 4 12 474.2 74.3 668 4 13 470.6 73.8 8501 6	2 99.2 638 6 2 99.2 638 6 3 99.3 638 9 9.3 1073 9 9.4 3 2259 9 8 86.2 638 6 8 86.2 638 6
	us e	08499 08297 R428605 08481449 08328 08328 08329 080329 080369 080669 080669 080770 080770 080757 080675 080757 0807	RJ80845 SAFGF OVFGFAA TEDGF 49428	02042 08496 WHECCEB C032697 SHPGF1 08190 99138
Drohan,W. Man endothelial cell growth Prussia, PA	linear PAT 21-MAY-1993	Sequence Sequence 49 Sequence 49 Sequence 601 Mus mus 601 Mus mus 60 Mus mus 601 Mus mus 60 Mus mus		102042 Sequence 5 108496 Sequence 7 M13361 Human beta- BC032697 Homo sapi X51943 Human mRNA 108090 Sequence 4 109138 Sequence 4 109138 Sequence 3 X13321 Bovine mRNA

28: gb_gssl:* 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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				: 5		Description
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u ,	560.8	87.9	878	22	B1753845	BM809005 AGENCOURT BI751845 601027526
י ו	559.8		821	5	B1598390	BI598390 603250094
o 8 7	501.6	80.2 78.6	534 714	3 9	NI590078	~
n			472	۰:	AI077609	BG706412 602669744 AI077609 0y26d02 8
11	434.6	68.1	3404	; ;	AX035330	۰,
12 1		66.5	461	5 5	BF956865	603
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15	408.2	64.0	663	, v	AI119291	AI119291 ue95c07.y
	402.2	63.0	750	13	BI331990 BU627243	60298439
	401.2	62.9	508	29	CG633840	BU627243 UI-H-FG0~ CG633840 OST353987
1 16	385.4	60.4	526	29	CG565930	05719113
20 5	385.2	60.4	631	٦ ۵		BB627624 BB627624
21	356	55.8	813	5	BF532970	AI663400 uk32d07.y
	354.6	55.6	119	IJ	BU840197	BU840197 AGENCOURT
24	327.4	51.3	203	5 5	BP958824	
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27	316.8	49.7	529	29	CD701495	
28	316.6		543	9	AA261582	AA261582 mz87c09.r
c 30	302	47.3	701	2 2	BM995210	CB773841 AMGNNUC:S
3 2	298.8	46.8	469	5 6	AW259195	
33	291.4		570	7 1	BI598882	BI598882 603247981
0 13 15 15	280.6	4 4 .	120	; •	AA594274	AA594274 nl90g01.s
c 36	279		115	9 5	MI083919	BX488304 DKPZp686G
بر 7 م	274.2	3.0	858	7	55	R54255 yg74£06.r1
9 6	273.6	42.9	424	14	MZ3109	R23109 xms1#12 21
2 6	267.4	11.9	384		AA238828	AA238828 mx92h02.r
ក ជំ	261.8	41.0		5 6	B8629001	BB629
	251.8			29	CG613113	CG613113 OCT299916
4 5 4	247 246	38.7 38.6	909 96	10 29	BB850804 CG496943	
						COMPAGNA CO17/4/0
					ALIGNMENTS	
RESULT 1 BX444567						
LOCUS DEFINITION		1567 1567 Homo	ō	9	1173 bp mRNA linear	linear EST 15-MAY-2003
ACCESSION		CSODNOO3YP16 BX444567	v	Ē	mRNA sequence.	
VERSION	BX44	BX444567.1	GI:30780253	3025	ະ	
SOURCE		sapiens	(human)	٤		
OX CHANGE OF		eapier	Metazoa.			
252555VC	· 	. m	Eutheria;	•	s, Catarrhini;	; Hominidae; Komo.
AUTHORS		W.B., Gru	ber, C.,	ພັ	.4	·
JOURNAL	-		gth cDNA libraries hed (2001)	bra	ries and normalization	В
TABIMMO		Contact: Genoscope	oscope			

of months

RESULT 2 BI869731 LOCUS

BI869731

832 bp

nRNA

linear

EST 11-OCT-2001

Genoscope - Centre National de Sequencage
BP 191 91016 EVRY cedex - Prance
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3201.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSODN003DH08QP1ccluster=3201.r. Contact:
Feng Liang Email: filangelifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen.Corporation 1600
FEATURES

1. 1173
/organism="Homo sapiens"
/mol_type="makla"
/db_xrefs"taxon:9606"
/clone="CSODN003TP16"
/tissue_type="ADULT BRAIN"
/dev_stage="Adult"
/dcw_stage="Adult"
/clone_ind="Organism= brain; Vector: pCNVSPORT_6; lst strand cDNA
vas primed with a Not1-oligo(df) primer. Five prime end
enriched, double-everand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCNVSPORT 6
vector. Library was not normalized."

δ 문 ð 문 S 片 Ş ₽ S 片 S 庆 र्ठ 문 ঠ 밁 밁 S \$ Query Match
94.3%; Score 601.8; DB 13; Length 1173;
Best Local Similarity 98.6%; Pred. No. 6.9e-166;
Matches 628; Conservative 0; Mismatches 7; Indels 2; Gaps 602 ACCCCCAGCCCACAGAGCCTGAATTTGTAAGCAACTT 638 612 552 AATGGGAGCTGCAAACGCGGTCCTCGGACTCACTATGGCCAGAAAGCAATCTTGTTTCTC 363 TACAACACCTATATATCCAAGAAGCATGCAGAGAAGAATTGGTTTGTTGTCCCCCCAAGAAG 422 68 372 312 183 123 CTCTACTGTAGGAAGGGGGGCCACTTCCTGAGGATCCTTCCCGGATGGCACAGTGGATCGG 182 252 192 63 CCCCTGCCAGTCTCTCTGATTAAAGAGATCTGTTCTGGGTGTTGACCACTCCAGAGAAG CCCCTGCCAGTCTCTCTGATTAAAGAGATCTGTTCT-GGTGTTGACCACTCCAGAGAAG GTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGGCCTTTTA 431 TTCACAGCCCTGACCGAGAAGTTTAATCTGCCTCCAGGGAATTACAAGAAGCCCAAACTC 122 ACAAGGGACAGGAGCGACACATTCAGCTGCAGCTCAGTGCGGAAAGCGTGGGGGAG ACAAGGGACAGGACCAGCACATTCAGCTGCAGCTCAGTTCCGGAAAGCGTTGGGGAG CTCTACTGTAGCAACGGGGCCACTTCCTGAGGATCCTTCCGGATGGCACAGTGGATGGG 671 541 611 371 242 311

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Score Match Length DB ID

Description

Run on: OM nucleic - nucleic search, using sw model

August 24, 2004, 20:02:52; Search time 4175 Seconds (without alignments) 6623.438 Million cell updates/sec

Title: Perfect score: Sequence: US-10-022-554A-3 638 1 gaattegggaaegegeeaca.....cetgaatttgtaageaaett 638

Scoring table: OLIGO_NUC Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: Word size : 0

6940544

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl: •

gb_ba.
gb_in.
gb_om.
gb_om.
gb_om.
gb_opat.

em ba: em fun: em in: em in: em on: em or: em pat: em ph:

em_sts:

em_htg_hum:*
em_htg_inv.*
em_htg_other:*
em_htg_mam:*
em_htg_pln:*
em_htg_rod:*
em_htg_ram:*
em_htg_vrt:*

em_htgo_hum, *
em_htgo_mus; *
em_htgo_other; *

SUMMARIES

Result

Query

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

9 HUMHBGP1 9 AC005370 2 AC091822 2 AC010489 2 AC016560 6 A00069
6 M4941449 6 109499 6 109499 6 120526 6 826510 6 837985 6 838005 6 826522 6 826529 6 826529 6 826521 6 826521 6 826529 6 826521 6 826529 6 826521 6 826529 6
AXX AXX AXX AXX E 22A E
ARRA ARRA ARRA ARRA ARRA ARRA ARRA ARR
s67991 Homo sapien ARA18605 Sequence ARA18605 Sequence ARA18605 Sequence A19428 Sequence 1 108499 Sequence 1 108499 Sequence 1 109297 Sequence 10 E37983 Process for E37984 Process for E37984 Process for E37984 Process for E37985 Process for E37987 Sugar chain E26527 Sugar chain E26528 Sugar chain E3603 Process for E37985 Sequence E38004 Process for E38007 Process for E380

ALIGNMENTS

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RSFERBNCS AUTHORS TITLS RESULT 1
102042
LOCUS
DEPINITION
ACCESSION
VERSION
VERSION ORIGIN SOURCE ORGANISM PEATURES JOURNAL source Unknown. Patent: US 4868113-A 5 19-SEP-1989; Rorer Biotechhology, Inc.; King of Prussia, PA Location/Qualifiers 1. .638 1 (bases 1 to 638) Jaye, H.. Burgess, W., Maciag, T. and Drohan, W. Recombinant DNA vector encoding human endothelial cell growth 638 bp 88-DNA Sequence 5 from Patent US 4868113. 102042 Unclassified. factor I02042.1 GI:270417 /organism="unknown"
/mol_type="unassigned_DNA" linear PAT 21-MAY-1993

Query Match 76.0%; Score 485; DB 6; Length 638; Best Local Similarity 99.5%; Pred. No. 1.2e-250; Matches 635; Conservative 0; Mismatches 3; Indels ç,

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and is derived by analysis of the total score distribution.

Homo sapiens	ORGANISM	Frocurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,	David N. Lo	urement.	one Proc	118810		
EST.	KEYWORDS	D.	Contact: Robert Strausberg, Ph.D. Smail: cgapbs-remail.nih.gov	bert St	ll cgap	Emai	COMPANY	_
BI598390	ACCESSION		Gene Index	(1998)	Unpublished (1998)	יקום. המקור	JOURNAL	
	DEFINITION	National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project	stitute / Nat	ind Stro	ional Ca	Disc	TITLE	
	RESULT 2 BI598390	(NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	pi//www.ncbi	(bases 1 to 534) /NINDS-CGAP http	(bases)	NCI,	REPERENCE AUTHORS	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Chordata;	Metazoa	aryota;			
110 GCAAACGCGC	Дb		n)	sapiens (human)	Homo sapiens Homo sapiens		SOURCE ORGANISM	
433 GCAAACGCGC	Ą		9126	GI:4599126	AI590078.1 EST.	AIS9	KEYWORDS	
170 ATATATCCA	40		uence.	mRNA sequence	AI590078	A15	ACCESSION	
373 ATATATCCA	Ş	similar to gb:M13361 HEPARIN-BINDING GROWTH FACTOR PRECURSOR 1	61 HEPARIN-B	E E TW: q6	ilar to			
230 AGACACCAA	рь	mRNA linear EST 21-APR-1999	534 b	3	AIS90078		LOCUS	
313 AGACACCAA	δ)	RESULT 1	
290 AGAGTACCG	9	ENTS	ALIGNMENTS					
253 AGAGTACCG	Q							
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193 GGAGCGACC	Ş				9.2	5 S	: ::	
	?	87234021 BY234021	13 BY230638	368	9.2	59	ដំ	
410 GCMACGGGG	핪	BY302462 BY302462		358		, U	2 6	
133 GCAACGGG	Q	CG620633 OST317992 AV141729 RV141729	29 CG620633 13 BY141229	344	9.2	59	39	
470 TGACCGAGA	Db	EG00210 051281652		344	9.2	59	33	
		CG496943 OST37278	29 CG496943	309	9 9	59	36	
	?	CG558760 OST175686	29 CG558760	242	9.2	59	2	
530 GCGCCACAA	Ę	BX501193 DKPZD779H		864	11.0	2 2	# #	
	?	BQ006000 UI-H-EI1-	12 BQ006006 9 AI359575	364	11.1	2 2		
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``		BF956865	_	461	45.8	292	9	
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rce 1	source	B1869731	12 BI869731	832 522	49.7	317	7 0	
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Insert Len		B1598390			68.0	434	ب اد	
found thro		AI590078 tm58c01.x	9 AIS90078		0.89	434	c 1	
Clone dis		Description	DB ID	Length	:	Score	No.	
cDNA Libr					Query		Result	
1					-			

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Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Mashington University Genome Sequencing Center
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CDNP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Organisms*Homo sapiens*
//Wol_types*MANA*
//Mol_types*MANA*
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//Lisue_types*Manaplastic oligodendroglioma*
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ity sequence stop: 455.
Location/Qualifiers
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GI:15491329
                                                                                                               821 bp mRNA linear EST 07-SEP-2001
NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5302030 5',
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100.0%; Pred. No. 2.2e-211;
stive 0; Mismatches 0; Indels
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and is derived by analysis of the total score distribution.

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*2:2588	ERRORA	EFF:SFAR	ERKERATA	EERAFRER	221 - 25 4 3	****	*******		22222	:::::	* # # #	2222	2222	2222	::::	2152	==-	, ,		
REQUESTE PROM M.A. HILLIMA.92102857, P. LI T.L., Exa M. Oc. Turck S.J., "An acidic Elbroble splicing acts like . J. Exp. Mad. 175:10	A LINE SI	SEQUENCE PRO MEDING-9007 Mergia h. T Mergia h. T Mergia h. T Mergia h. T Mergia h. T Siochem. Biq [3]	ASQUINCE PROM M. TISSUM-Brain see REMINE-SOISSELS Chiu I.M., wang 'alternative sp) Asparin-binding Oncogene \$1759-1 [6]	#EQUINCE PROM TISTIN-Brain = MEDINE-893431 Wang W.P., Lab Wang M.P., Lab "Cloming of th factor and its Pol. Coll. Sio [3]	HERLIES FROM M.A. HERLIES-655105; PAMPA Juye M., Noch R., Bung O'Brien S.J., Noch M.S. 'Emman enderballal call and chromosome localist Boisnes 333:541-545[1]	aryota,	TI MUNAN POSIJO, PO 11-AUG-1981 11-AUG-1981 13-EEP-2001 Meparin-bis Growth fact beca).		199.5	302		211.5 211.5 211.5				5 .3 3		200	7 2 8 2	1697
OF M.A. OZSKY, P A.R., Oc Elbroble Calle L. 175:10	Oulek D., Oulek D., d sequence and ite; 1821-1829	Tiocher Canlysi		All stand	100 H.A.	Hetazon Hetazon Uchecia	W STAND 107502; 107 (Bal. of 107 (Bal. 85 100) (Bal. 85 10			::::		2223								10.
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